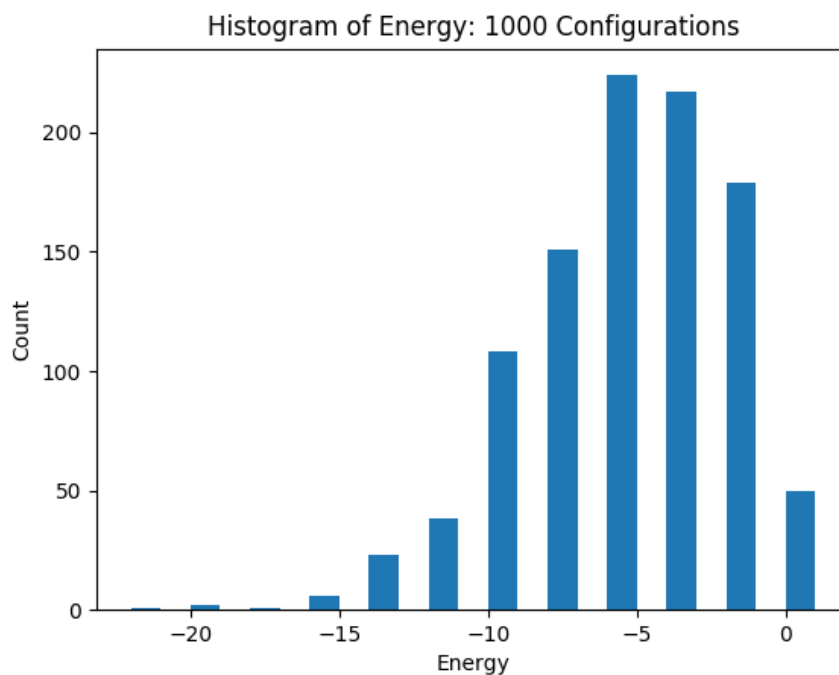


## PART A

In this section we were asked to read in a file containing a sequence of H and P representing hydrophobic and polar amino acids forming a protein. Additionally, we were asked to build a lattice model to obtain a folded protein configuration and to calculate the energy of the configuration. In my methods, I utilize the **folding**, **calc\_energy**, and **get\_new\_pos** functions I have written to accomplish this.

## PART B

In this section, we were asked to implement the metropolis algorithm to simulate a population of configurations that obey the Boltzmann distribution. I accomplished this by utilizing my function **simulate**, which calls my functions **reconfig** and **calc\_energy**. Below is the histogram of 1000 iterations, with temperature set to 100. Here we observe that there are only even number energies calculated. This is because in the **calc\_energy** function I double count each topological neighbor's energy.



## PART C

In this section, we were asked to optimize our configurations to have the lowest possible energy. Here, we implement the simulated annealing and the metropolis algorithm. First, I initialized a population of random configurations with size = 100. I changed the population size from very small to large and found that larger population sizes yield better optimized configurations and a lower best energy. However, code for larger population sizes take significantly longer to run.

I then chose a random member of this population and created a second generation that will be equal or smaller in size. A random member from this generation is then chosen and a new generation is generated. This process is repeated until our generation size = 1 or 0 OR the temperature has reached 0. Through all this, each legitimate child that is produced in a generation is checked whether it has a lower energy than our current lowest known configuration energy. Children are passed on to a new generation if their energy is deemed appropriate PH\_AI.py (lines 376-383). Sometimes, we allow some children with higher energies than their parent so that we may be able to overcome being in a local min of the distribution and find a lower energy. The lowest energy for a configuration that I was able to find through this method is -28. The corresponding lattice configuration can be seen on the next page.

**Optimized Configuration (protein index, lattice position)**

0,"[0, 0]"	18,"[6, 2]"	36,"[11, 9]"	54,"[8, 8]"	72,"[11, 15]"
1,"[1, 0]"	19,"[6, 3]"	37,"[11, 10]"	55,"[8, 7]"	73,"[12, 15]"
2,"[1, 1]"	20,"[6, 4]"	38,"[11, 11]"	56,"[7, 7]"	74,"[12, 16]"
3,"[0, 1]"	21,"[6, 5]"	39,"[11, 12]"	57,"[7, 8]"	75,"[12, 17]"
4,"[0, 2]"	22,"[6, 6]"	40,"[11, 13]"	58,"[7, 9]"	76,"[12, 18]"
5,"[0, 3]"	23,"[7, 6]"	41,"[10, 13]"	59,"[6, 9]"	77,"[12, 19]"
6,"[1, 3]"	24,"[7, 5]"	42,"[10, 12]"	60,"[6, 10]"	78,"[12, 20]"
7,"[1, 2]"	25,"[7, 4]"	43,"[10, 11]"	61,"[6, 11]"	79,"[13, 20]"
8,"[2, 2]"	26,"[8, 4]"	44,"[10, 10]"	62,"[7, 11]"	80,"[13, 21]"
9,"[3, 2]"	27,"[8, 5]"	45,"[9, 10]"	63,"[7, 12]"	81,"[13, 22]"
10,"[4, 2]"	28,"[8, 6]"	46,"[9, 11]"	64,"[7, 13]"	82,"[13, 23]"
11,"[4, 1]"	29,"[9, 6]"	47,"[9, 12]"	65,"[7, 14]"	83,"[13, 24]"
12,"[4, 0]"	30,"[9, 7]"	48,"[9, 13]"	66,"[8, 14]"	84,"[13, 25]"
13,"[4, -1]"	31,"[9, 8]"	49,"[8, 13]"	67,"[9, 14]"	85,"[13, 26]"
14,"[5, -1]"	32,"[9, 9]"	50,"[8, 12]"	68,"[9, 15]"	
15,"[5, 0]"	33,"[10, 9]"	51,"[8, 11]"	69,"[10, 15]"	
16,"[6, 0]"	34,"[10, 8]"	52,"[8, 10]"	70,"[10, 14]"	
17,"[6, 1]"	35,"[11, 8]"	53,"[8, 9]"	71,"[11, 14]"	